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(54) **Method for obtaining information regarding quantity of DNA after non-methylated cytosine converting treatment in analysis of DNA methylation**

(57) The present invention provides an easy and accurate method for obtaining information regarding a quantity of DNA included in a sample used for analyzing a methylation of a target DNA, comprising steps of: treating a biological sample containing DNA including the target DNA with a non-methylated cytosine converting

agent for converting non-methylated cytosine of the DNA into another base; and obtaining information regarding a quantity of DNA included in the sample treated in the treating step by using an oligonucleotide complementary to a cytosine-free region of the target DNA.

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DOCUMENTS CONSIDERED TO BE RELEVANT			
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (IPC)
X	GRUNAU C ET AL: "Bisulfite genomic sequencing: systematic investigation of critical experimental parameters" NUCLEIC ACIDS RESEARCH, OXFORD UNIVERSITY PRESS, SURREY, GB, vol. 29, no. 13, 1 January 2001 (2001-01-01), pages e65-1, XP002241346 ISSN: 0305-1048 * the whole document *	1-20	INV. C12Q1/68
A	WOJDACZ TOMASZ K ET AL: "Techniques used in studies of age-related DNA methylation changes" ANNALS OF THE NEW YORK ACADEMY OF SCIENCES, NEW YORK ACADEMY OF SCIENCES, NEW YORK, NY, US, vol. 1067, 1 May 2006 (2006-05-01), pages 479-487, XP009116695 ISSN: 0077-8923 * abstract *		TECHNICAL FIELDS SEARCHED (IPC)
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The present search report has been drawn up for all claims			
Place of search Munich		Date of completion of the search 26 May 2009	Examiner Leber, Thomas
CATEGORY OF CITED DOCUMENTS X : particularly relevant if taken alone Y : particularly relevant if combined with another document of the same category A : technological background O : non-written disclosure P : intermediate document		T : theory or principle underlying the invention E : earlier patent document, but published on, or after the filing date D : document cited in the application L : document cited for other reasons & : member of the same patent family, corresponding document	

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A	LEWIN J\RN ET AL: "Quantitative DNA methylation analysis based on four-dye trace data from direct sequencing of PCR amplificates" BIOINFORMATICS, OXFORD UNIVERSITY PRESS, SURREY, GB, vol. 20, no. 17, 22 November 2004 (2004-11-22), pages 3005-3012, XP002467526 ISSN: 1367-4803 * abstract *		
A	LEHMANN U ET AL: "Real-Time PCR-Based Assay for Quantitative Determination of Methylation Status" METHODS IN MOLECULAR BIOLOGY, HUMANA PRESS INC., CLIFTON, NJ, US, vol. 287, 1 January 2004 (2004-01-01), pages 207-218, XP003015589 ISSN: 1064-3745 * page 209 - page 210 *		TECHNICAL FIELDS SEARCHED (IPC)
A	WARNECKE PETER M ET AL: "Identification and resolution of artifacts in bisulfite sequencing" METHODS : A COMPANION TO METHODS IN ENZYMOLOGY, ACADEMIC PRESS INC., NEW YORK, NY, US, vol. 27, no. 2, 1 June 2002 (2002-06-01), pages 101-107, XP002410143 ISSN: 1046-2023 * page 102, left-hand column *		
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A	SO KANJI ET AL: "Quantitative assessment of RUNX3 methylation in neoplastic and non-neoplastic gastric epithelia using a DNA microarray." PATHOLOGY INTERNATIONAL OCT 2006, vol. 56, no. 10, October 2006 (2006-10), pages 571-575, XP009116724 ISSN: 1320-5463 * page 573, left-hand column *		
A	TUSNÁDY GÁBOR E ET AL: "BiSearch: primer-design and search tool for PCR on bisulfite-treated genomes." NUCLEIC ACIDS RESEARCH 2005, vol. 33, no. 1, 2005, page e9, XP009116757 ISSN: 1362-4962 * the whole document *		TECHNICAL FIELDS SEARCHED (IPC)
The present search report has been drawn up for all claims			
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